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---MKKMSPYQNKNEYEILESSSNNTNTPNRYP---FANNRDMSTMS-----WNDCQGI 48
axmi008
              ------VEVL 24
crylAa
              -----VEVL 24
cry1Ac
              ------MKLKNQDKHQSFSSNAKVDKISTDS---LKNETDIELQNINHEDCLKMSEYE 49
crylIa
              -----MNNVLNSGRTTICDAYNVVAHDPFSFEHKSLDTIQKEWMEWKRTDHSLYVAPVV 54
cry2Aa
              MIRKGGRKMNPNNRSEHDTIKTTENNEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADN 60
cry3Aa1
              ------MNPNNRSEHDTIKVTPNSELQTNHNQYPLADNPNSTLEELNYKEFLRMTEDS 52
cry3Bb
              -----MNPYQNKNEYETLNASQKKLNISNNYTRYPIENSPKQLLQSTNYKDWLNMCQQN 54
cry4Aa
              -----MN------SGYPLANDLQGSMKNTNYKDWLAMCENN 30
cry4Ba
              ------MIIDSKTTLPRHSLIHTIKLNSNKKYGPGDMTNGNQFIISKQEWATIGAYI 51
cry6Aa
              -----TQKALSPSLKNMNYQDFLSITERE 47
cry7Aa
              ------MSPNNQNEYEIIDATPSTSVSSDSNRYPFANEPTDALQNMNYKDYLKMSGGE 52
cry8Aa
              -----MNPYQNKNEYEIFNAPSNGFSKSNNYSRYPLANKPNQPLKNTNYKDWLNVCQDN 54
cry10Aa
              -----MHYYGNRNEYDILNASSNDSNMSNTYPRYPLANPQQDLMQNTNYKDWLNVCEGY 54
cry16Aa
              -----MNSYQNKNEYEILDAKRNTCHMSNCYPKYPLANDPQMYLRNTHYKDWINMCEEA 54
cry19Ba
              -----MNQYQNKNEYEILESSQNNMNMPNRYP---FADDPNAVMKNGNYKDWVNECEGS 51
cry24Aa
              ----- MNPYQNKSECEILNAPLNNINMPNRYP--- FANDPNAVMKNGNYKDWLNECDGI 51
crv25Aa
              -----NSYENKNEYEILNDSKK-SNMSNPYLRYPLANDSLASMQNTNYKDWLTMCDRT 52
cry39Aa1
               ------NSYENKNEYEILESSSNNTNMPNRYP---FANDRDMSTMS-----FNDCQGI 44
cry40Aa1
              S-----WDEIWESVETITSIGINLIEFVIEPSLGGINTLLSIIGKLIPTNRQT- 96
axmi008
              G-----GERIETGYTPIDISLSLTQFLLS-EF-VPGAGFVLGLVDIIWGIFGPSQ--- 72
cry1Aa
              G------GERIETGYTPIDISLSLTQFLLS-EF-VPGAGFVLGLVDIIWGIFGPSQ--- 72
cry1Ac
              N-----VEPFVS-ASTIQTGIGIAGKILG-TLGVPFAGQVASLYSFILGELWP-KGK- 98
cry1Ia
              G------KRILSELWGIIFPSGSTN 88
cry2Aa
             N-----TEALDSSTTKDVIQKGISVVGDLLG-VVGFPFGGALVSFYTNFLNTIWPSE--- 111
cry3Aa1
              S----TEVLDNSTVKDAVGTGISVVGQILG-VVGVPFAGALTSFYQSFLNTIWPSDA-- 104
cry3Bb
              QQYGGDFETFIDSG---ELSAYTIVVGTVLTGFGFTTPLGLALIGFGTLIPVLFPAQDQS 111
cry4Aa
              QQYG-VNPAAINSS---SVSTALKVAGAILK--FVNPPAGTVLTVLSAVLPILWPTNTPT 84
cry4Ba
             O-----TGLGLPVNEQQLRTHVNLSQDISIPSDFSQLYDVYCSDKTS- 93
cry6Aa
             O-----PEALASGNTAINTVVSVTGATLS-ALGVPGASFITNFYLKIAGLLWPENGK- 98
cry7Aa
             NPEL-FGNPETFIS-SSTIQTGIGIVGRILG-ALGVPFASQIASFYSFIVGQLWPSKSV- 108
cry8Aa
              QQYGNNAGNFASSETIVGVSAGIIVVGTMLG-AFAAPVLAAGIISFGTLLPIFWQGSDPA 113
cry10Aa
              -----HIENPREASVRAGLGKGLGIVSTIVGF-FGGSIILDTIGLFYQISELLWPEDDT- 107
cry16Aa
              ----SYASSGPSQL---FKVGGSIVAKILG-----MIPEVGPLLSWMVSLFWPTIEE- 99
cry19Ba
              N-----ISPSPAAAITSKIVSIVLKTLAKAVASSLADSIKSSLGISKTITENN- 99
cry24Aa
              T-----PSIFGTLGVLASIVISTIN-LATSPSIGDAFALVSSIGEYWPETKTS- 98
cry25Aa
               ----DTDVLSSRGA---VSTGVGMLSTILSL-FGIPLIGEGIDLLLGAADFLWPESDGG 103
cry39Aa1
               cry40Aa1
               ---VSALSICDLLSIIRKEVADSVLSDAIADF-DGKLKNYREYYLSYLGAWLKDGKPLQK 152
axmi008
               ----WDAFPVQIEQLINQRIEEFARNQAISRL--EGLSNLYQIYAESFREWEADPT---N 123
cry1Aa
               ----WDAFLVQIEQLINQRIEEFARNQAISRL--EGLSNLYQIYAESFREWEADPT---N 123
cry1Ac
              --NQWEIFMEHVEEIINQKISTYARNKALTDL--KGLGDALAVYHDSLESWVGNRN---N 151
cry1Ia
              ---LMQDILRETEQFLNQRLNTDTLARVNAEL--IGLQANIREFNQQVDNFLNPTQNPVP 143
cry2Aa
              --DPWKAFMEQVEALMDQKIADYAKNKALAEL--QGLQNNVEDYVSALSSWQKNPVSSRN 167
cry3Aa1
              --DPWKAFMAQVEVLIDKKIEEYAKSKALAEL--QGLQNNFEDYVNALNSWKKTPLSLRS 160
cry3Bb
              --NTWSDFITQTKNIIKKEIASTYISNANKIL--NRSFNVISTYHNHLKTWENNPNPQ-N 166
cry4Aa
             PERVWNDFMTNTGNLIDQTVTAYVRTDANAKM--TVVKDYLDQYTTKFNTWKREPNNQSY 142
cry4Ba
              -AEWWNKNLYPLIIKSANDIASYGFKVAGDPS--IKKDGYFKKLQDELDNIVDNNS---- 146
cry6Aa
               --I-WDEFMTEVEALIDQKIEEYVRNKAIAEL--DGLGSALDKYQKALADWLGKQD---D 150
cry7Aa
               --DIWGEIMERVEELVDQKIEKYVKDKALAEL--KGLGNALDVYQQSLEDWLENRN---D 161
cry8Aa
              N--VWQDLLN-IGGRPIQEIDKNIINVLTSIV--TPIKNQLDKYQEFFDKWEP-ARTHAN 167
cry10Aa
               QQYTWQDIMNHVEDLIDKRITEVIRGNAIRTL--ADLQGKVDDYNNWLKKWKDDPKSTGN 165
cry16Aa
               KNTVWEDMIKYVANLLKQELTNDTLNRATSNL--SGLNESLNIYNRALAAWKQNKNNFAS 157
cry19Ba
               ---VSQVSMVQVHQIINRRIQETILDLGESSL-NGLVAIYNRDYLGALEAWNNN-----K 150
crv24Aa
               ----FPLSVADVNRLIREALDQNAINRATGKFN-GLMDTYNTVYLKNLQDWYDTRIPANP 153
cry25Aa
               HQYTWEDLMNHIEELMDERLETEKRTTALDDL--RGLKALLGLFRDAFDSWEKNQNDPIA 161
cry39Aa1
               ---VSALSICDLLSIIRKEVADSVLSDAICRFLDGKLKNYREYYLPYLEAWLKDGKPLQK 149
cry40Aa1
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TNNSDI-GQLVYYFKLSERDFNEILGGSLSRN-----NAQVLLLPTFAQAANVQLLLLRD 206
axmi008
              PALR---EEMRIQFNDMNSALTTAIPLLAVQ-----NYQVPLLSVYVQAANLHLSVLRD 174
crylAa
              PALR---EEMRIQFNDMNSALTTAIPLFAVQ-----NYQVPLLSVYVQAANLHLSVLRD 174
cry1Ac
              TRAR---SVVKSQYIALELMFVQKLPSFAVS-----GEEVPLLPIYAQAANLHLLLLRD 202
cry1Ia
              LSIT-----SSVNTMQQLFLNRLPQFQIQG-----YQLLLLPLFAQAANMHLSFIRD 190
cry2Aa
              PHSQ---GRIRELFSQAESHFRNSMPSFAIS-----GYEVLFLTTYAQAANTHLFLLKD 218
cry3Aa1
              KRSQ---DRIRELFSQAESHFRNSMPSFAVS-----KFEVLFLPTYAQAANTHLLLLKD 211
cry3Bb
              TQDV---RTQIQLVHYHFQNVIPELVNSCPPNPSDCDYYNILVLSSYAQAANLHLTVLNQ 223
cry4Aa
              RTAV---ITQFNLTSAKLRETAVYFSNLVG------YELLLLPIYAQVANFNLLLIRD 191
cry4Ba
              -----DDDAIAKAIKDFKARCG-----ILIKEAKQYEEAAKNIVTSLD 184
cry6Aa
              PEAI---LSVATEFRIIDSLFEFSMPSFKVT-----GYEIPLLTVYAQAANLHLALLRD 201
cry7Aa
              ARTR---SVVSNQFIALDLNFVSSIPSFAVS-----GHEVLLLAVYAQAVNLHLLLLRD 212
cry8Aa
              AKAV---HDLFTTLEPIIDKDLDMLKNNAS-------YRIPTLPAYAQIATWHLNLLKH 216
cry10Aa
              LSTL---VTKFTALDSDFNGAIRTVNNQGSP-----GYELLLLPVYAQIANLHLLLLRD 216
cry16Aa
              GELI---RSYINDLHILFTRDIQSDFSLG------GYETVLLPSYASAANLHLLLLRD 206
cry19Ba
              SNINYQ-TNVAEAFKTVEREFFTKLKGIYRTS----SSQITLLPTFTQAANLHLSMLRD 204
cry24Aa
              QGDSQLREAARRSLEEIERDFRKALAGEFAEAG-----SQIVLLPIYAQAANIHLLILKD 208
cry25Aa
              KNRV---GGYFEDVHTHFVKDMASIFSAT-----NYEVLLLPVYAQAANLHLLLLRE 210
cry39Aa1
              TNNSDI-GQLVKYFELSERDFNEILGGSLARN-----NAQILLLPYFCASCKCQLLLLRD 203
cry40Aa1
              AVQYKAQWFPFLSAENVRSELISPNSGCDFTGDYYERLKCKTAEYTNYCLYWYQVGLNQI 266
axmi008
              VSVFGQRWGFDAAT-----INSRYNDLTRLIGNYTDYAVRWYNTGLERV 218
cry1Aa
              VSVFGQRWGFDAAT------INSRYNDLTRLIGNYTDYAVRWYNTGLERV 218
cry1Ac
              ASIFGKEWGLSSSE-----ISTFYNRQVERAGDYSDHCVKWYSTGLNNL 246
crylIa
              VILNADEWGISAAT-----LRTYRDYLRNYTRDYSNYCINTYQTAFRGL 234
cry2Aa
              AQIYGEEWGYEKED------IAEFYKRQLKLTQEYTDHCVKWYNVGLDKL 262
cry3Aa1
              AQVFGEEWGYSSED------VAEFYHRQLKLTQQYTDHCVNWYNVGLNGL 255
cry3Bb
              AVKFEAYLKNNRQFDYLEP------LPTAIDYYPVLTKAIEDYTNYCVTTYKKGLNLI 275
crv4Aa
              G-----LINAQEWSLAR------SAGDQLYNTMVQYTKEYIAHSITWYNKGLDVL 235
cry4Ba
              QFLHGDQKKLEGVIN-----IQKRLKEVQTALNQAHGESSPAHKELLEKV 229
cry6Aa
              STLYGDKWGFTQNN------IEENYNRQKKRISEYSDHCTKWYNSGLSRL 245
cry7Aa
              ASIFGEEWGFTPGE-----ISRFYNRQVQLTAEYSDYCVKWYKIGLDKL 256
cry8Aa
              AATYYNIWLQNQGINPST-----FNSSNYYQGYLKRKIQEYTDYCIQTYNAGLTMI 267
cry10Aa
              AQIYGDKWWSARAN-------ARDNYYQIQLEKTKEYTEYCINWYNKGLNDF 261
cry16Aa
              VAIYG-KELGYPST-----DVEFYYNEQKYYTEKYSNYCVNTYKSGLESK 250
cry19Ba
              AVMYQEGWNLQSHIN------YSKELDDALEDYTNYCVEVYTKGLNAL 246
cry24Aa
              AMQFRTDLGLIRPVGVPITTS-----AEDPFESEFLLRIKKYTDHCISYYDDGLAKI 260
cry25Aa
              GVIYG-SRWGIAP-------AADFYHDQLLKYTAIYANHCVTWYNNGLAQQ 253
cry39Aa1
              AVQYEEQWFPFLSAENVRSELISPNSGCDFTGDYYERLKCKIAEYTDYCEYWYQAGLNQI 263
cry40Aa1
              KQGGTGAD----TWSKFNKFRREMTLAVLDIIAIFPTYDFEKYPLP-----THVELTR 315
axmi008
              WGPDSR-----TVSQLTR 265
crylAa
              WGPDSR-----TVSQLTR 265
cry1Ac
              RGTNAE-----SWVRYNQFRRDMTLMVLDLVALFPSYDTQMYPIK-----TTAQLTR 293
crylIa
              NT------RLHDMLEFRTYMFLNVFEYVSIWSLFKYQSLMVS-----SGA 273
cry2Aa
              RGSSYE-----SWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKE-----VKTELTR 309
cry3Aa1
              RGSTYD-----AWVKFNRFRREMTLTVLDLIVLFPFYDIRLYSKG-----VKTELTR 302
cry3Bb
              KTTPDSNLDGNINWNTYNTYRTKMTTAVLDLVALFPNYDVGKYPIG-----VQSELTR 328
cry4Aa
              RNKSNG-----QWITFNDYKREMTIQVLDILALFASYDPRRYPADKIDNTKLSKTEFTR 289
cry4Ba
              KN-----FVVY 265
cry6Aa
              NGSTYE-----QWINYNRFRREMILMALDLVAVFPFHDPRRYSME-----TSTQLTR 292
cry7Aa
              KGTTSK-----SWLNYHQFRREMTLLVLDLVALFPNYDTHMYPIE-----TTAQLTR 303
cry8Aa
              RTNTNA-----TWNMYNTYRLEMTLTVLDLIAIFPNYDPEKYPIG------VKSELIR 314
cry10Aa
              R-----TAGOWVNFNRYRREMTLTVLDIISMFPIYDARLYPT-----EVKTELTR 306
cry16Aa
              K-----QIG-WSDFNRYRREMTLSVLDIVALFPLYDTGLYPSK--DGKIHVKAELTR 299
cry19Ba
              R--GSTAI----DWLEFNSFRRDMTLMVLDLVAIFPNYNPVRYPLS-----TKISLSR 293
cry24Aa
              RSRGSDGE----TWWEFNKFRREMTLTVLDLVALYPTHNIKLYPIP-----TQTELSR 309
cry25Aa
              KE----LFAKSPNWNRFNAYRRDMTITVLDIIALFPTYDARLYTK-----PIKTELTR 302
cry39Aa1
              KOAGTGAD----TWAKFNKFRREMTLTVLDIIAIFQTYDFKKYPLP----THVELTR 312
cry40Aa1
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EIYTDAVGYSS----GTYSWLRNWPNTFNGLEANGTRGP-GLVTWLSKIGIYNEYVSRY 369
axmi008
              EIYTNPVLENFDGS-----FRG--MAQRIEQNIRQP-HLMDILNSITIYTDVHRGF 313
crylAa
              EIYTNPVLENFDGS-----FRG--SAQGIERSIRSP-HLMDILNSITIYTDAHRGY 313
cry1Ac
              EVYTDAIGTVHPHPSFTSTTWYNNNAPSFSAIEAAVVRNP-HLLDFLEQVTIYSLLS--R 350
cry1Ia
             NLYASGSGPQQTQS-----FTAQNWPFLYSLFQVNSNYILSGISGTRLSITFPNIG 324
cry2Aa
             DVLTDPIVGVNNLR------GYGTTFSNIEN-YIRKP-HLFDYLHRIQFHTRFQPGY 358
cry3Aa1
             DIFTDPIFSLNTLQ------EYGPTFLSIEN-SIRKP-HLFDYLQGIEFHTRLQPGY 351
cry3Bb
             EIYQVLN---FEES-----PYKYYDFQYQEDSLTRRP-HLFTWLDSLNFYEKAQTTP 376
cry4Aa
             EIYTAL----VES-----PSSK-SIAALEAALTRDV-HLFTWLKRVDFWTNTIYQD 334
cry4Ba
             EILENTAVQHIKNQ-----IDEIKKQLDSAQHDLDRDVKIIGMLNSINTDI 311
cry6Aa
             EVYTDPVSLSISNP------DIGPSFSQMENTAIRTP-HLVDYLDELYIYTSKYKAF 342
cry7Aa
              DVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVIRPP-HLFDILSSVEINTSRGGIT 362
crv8Aa
              EVYTNVN-----SDTFRTITELENGLTRNP-TLFTWINQGRFYTRNSRDI 358
cry10Aa
              EIYSDVINGEIYGL-----MTPYFSFEKAESLYTRAP-HLFTWLKGFRFVTNS-ISY 356
cry16Aa
              EIYSDVINDHVYGL------MVPYISFEHAESLYTRRP-HAFTWLKGFRFVTNS-INS 349
cry19Ba
              KIYTDPVGRTDSPS-FGDWTNTGRTLANFNDLEREVTDSP-SLVKWLGDMTIYTGAIDSY 351
cry24Aa
              VVYTDPVGCFGNRK-----SDIFSRLNFDYLENRLTRPR-EPFNYLNSVQLFASTVSNS 362
cry25Aa
              EIYSDVLNLDVYGV-----QQT--DLNKNEAAFTRSP-HLVTRLRGFDFYTRTKYAY 351
cry39Aa1
               EIYTDPVGYSS-----GTYSWLKYWTGAFNTLEANGTRGP-GLVTWLRSIGIYNEYVSRY 366
cry40Aa1
               FAG-----WVGTRHYEDYTKGNGIFQR------MSGTTSNDLRNIDFQ---NADV 410
axmi008
               N-----FGNAGNAAPP-VLVSLTGLGIF 358
crylAa
               Y-----YWSGHQIMASPVGFSGPEFTFPL-----YGTMGNAAPQQRIVAQLGQGVY 359
cry1Ac
               WSNTQYMN-MWGGHKLEFRTIGGTLNISTQ------GSTNTSINPVTLPFTSRDVY 399
crylIa
               GLPG----STTTHSLNSARVNYSGGVSSGLIG-----ATNLNHNFNCSTVLPPLSTPF 373
cry2Aa
               YGNDSFN--YWSGNYVSTRPSIGSNDIITSPF-----YGNKSSEPVQ--NLEFNGEKVY 408
cry3Aa1
               FGKDSFN--YWSGNYVETRPSIGSSKTITSPF-----YGDKSTEPVQ--KLSFDGQKVY 401
cry3Bb
              NN-----FFTSHYNMFHYTL-DNISQKSSV-----FGNHNVTDKLKS-LGLATNIYI 421
cry4Aa
             LR-----FLSANKIGFSYTN-SSAMQESGI-----YGSSGFGSNLTHQIQLNSNVYK 380
cry4Ba
              DN------LYSQGQEAIKVFQKLQGIWATIG--------AQIENLRTTSL 347
cry6Aa
              SHEIQPDLFYWSAHKVSFKKSEQSN-LYTTGI-----YGKTSGYISS-GAYSFHGNDIY 394
cry7Aa
              LNNDAYIN-YWSGHTLKYRRTADSTVTYTA------NYGRITSEKNSFALEDRDIF 411
cry8Aa
              LDPYDIF--SFTGNQMAFTHTN-DDRNIIWGA-----VHGNIISQDTSKVFPFYRNKPI 409
cry10Aa
               WT-----FLSGGQNKYSYTN-NSSINEGSF-----RGQDTDYGGTSSTINIPSNSYV 402
cry16Aa
               WT-----FLSGGENRYFLTHGEGTIYNGPF-----LGQDTEYGGTSSYIDISNNSSI 396
cry19Ba
              RPT-----SPGDRIGVWYGNINAFYHTGRTDVVMFRQTGDTAYEDPSTFISNILYDDI 404
cry24Aa
               NNGE-----VLRGNLNKIMFEGGWTASRSGDG----VTTGTPFSTMDWSYGWGYPRKHYA 413
cry25Aa
               WR-----YLAGHTNYFSFTG-NGTIYSSSF-----N-NWYDTDMTKSTINIPDYANI 396
cry39Aa1
               FSG-----MSGTTSNDLRDISFP---NSDI 407
cry40Aa1
               YKITSLAIMNLVGETTARPEYRVSKADFRRVGGPDLNYDAGNNGLSRMTIESTFPLVLHS 470
axmi008
               RTLSSP---LYRRIILGSGPNNQELFVLDGTEFSFASLTTNLPSTIYRQRGTVDSLDVIP 415
cry1Aa
               RTLSST---LYRRPFN-IGINNQQLSVLDGTEFAYG-TSSNLPSAVYRKSGTVDSLDEIP 414
cry1Ac
              RTESLAGLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFYYPGYAGIG--TQLQDSENELP 457
crylIa
               VRSWLDSGTDREGVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPDYFIRNISGVPLVI 433
cry2Aa
               RAVANTNLAVWPS-AVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVG-AVS-WDSIDQLP 465
cry3Aa1
               RTIANTDVAAWPNGKVYLGVTKVDFSQYDDQKNETSTQTYDSKRNNG-HVSAQDSIDQLP 460
cry3Bb
               FLLNVISLDNKY-LNDYNNISKMDFFITNGTRLLEKELTAGSGQITYDVNKNIFGLPILK 480
cry4Aa
               TSITDTSSP-----SNRVTKMDFYKIDGT---LASYNSNITPTPEGLRTTFFGFSTNE 430
cry4Ba
               QEVQDSDDADEIQIELEDASDAWLVVAQEARDFTLNAYSTNSRQNLPINVISDSCNCSTT 407
cry6Aa
               RTLAAPSVVVYPYTQN-YGVEQVEFYGVKGHVHYRGDNKYDL-----TYDSIDQLP 444
cry7Aa
               EINSTVANLANYYQKAYGVPGSWFHMVKRGTSSTTAYLYSKTHTALQGCTQVYESSDEIP 471
cry8Aa
               DKVEIVRHR-----EYSDIIYEMIFFSNSSE---VFRYSSNSTIENNYKRTDSYMIPKQT 461
cry10Aa
               YNLWTENYEYIYPWGDPVNITKMNFSVTDNNSSKELIYGAHRTNKPVVRTDFDFLTNKEG 462
cry16Aa
               YNLWTKNYEWIYPWTDPVNITKINFSITDNSNSSESIYGAERMNKPTVRTDFNFLLNRAG 456
cry19Ba
               YKLDLRAAAVSTIQGAMDTTFGVSSSRFFDIRGRNQLYQS-NKPYPSLPITITFPGEESS 463
cry24Aa
               EITSRSQALPGLNNSIHVIVGIDSFRAIGPGGQGDHTFSLPGGDMYDCGKVQINPLEDYR 473
crv25Aa
               YKLWTKSYTNISPYTDPVGISQMQFSLTNN---QQLTYTGTSAPKYPVRETF-FEIPPTD 452
cry39Aa1
               FKIESKAIMNLVGEINARPEYRVSRAEFSESTAFIYLYDAGNSGLSSMTITSKLPGIKNP 467
cry40Aa1
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| axmi008  | N-GVRGPSHRLSNAACVVYGNSRVNVYGWTHTSLKRENIIE                  | 510 |
|----------|--|-----|
| cry1Aa   | PQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAPTFSWQHRSAEFNNIIP        | 466 |
| cry1Ac   | PQNNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIA      | 467 |
| cry1Ia   | PEATGQPNYESYSHRLSHIGLISASHVK-ALVYSWTHRSADRTNTIE            | 503 |
| cry2Aa   | RNEDLTRPLHYNQIRNIESPSGTPGGARAYLVSVHNRKNNIYAANENGTMIHLA     | 487 |
| cry3Aa1  | PETTDEPLEKGYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVDFFNMID           | 513 |
| cry3Bb   | PETTDEPLEKAYSHQLNYAECFLMQDRRGTIPFFTWTHRSVDFFNTID           | 508 |
| cry4Aa   | RRENQGNPTLFPTYDNYSHILSFIKSLSIPATYKTQVYTFAWTHSSVDPKNTIY     |     |
| cry4Ba   | NTPNQPTVNDYTHILSYIKTDVIDYNSNRVSFAWTHKIVDPNNQIY             |     |
| cry6Aa   | NMTSNQYSNPTTNMTSNQYMI                                      |     |
| cry7Aa   | PDGEPIHEKYTHRLCHATAIFKSTPDYDNATIPIFSWTHRSAEYYNRIY          | 493 |
| cry8Aa   | LDRTVPVAESYSHRLSHITSHSFSKNG-SAYYGSFPVFVWTHTSADLNNTIY       |     |
| cry10Aa  | WKNEEYGHTLSYIKTDNYIFSVVRERRRVAFSWTHTSVDFQNTID              |     |
| cry16Aa  | TELAKYNDYNHILSYMLINGETFGQKRHGYSFAFTHSSVDPNNTIA             |     |
| cry19Ba  | NGPTTYNDYNHILSYMLINGETFGQKRHGYSFAFTHSSVDRYNTIV             |     |
| cry24Aa  | EGNANDYSHLLCDVKILQEDSSNICEGRSSLLSHAWTHASLDRNNTIL           |     |
| cry25Aa  | NSDHWISDMMTINQSVQLASNPTQTFAFSALSLGWHHSSAGNRNVYV            |     |
| cry39Aa1 | EKPLTYENYSHILSYMTS-AQHFGDKKIGYTFAWMHESVDFDNRVD             |     |
| cry40Aa1 | EPSYRDYSHRLSNAACVGAGNSRINVYGWTHTSMSKYNLIY                  | 508 |
|          |  |     |
|          |  |     |
| axmi008  | ANQITQIPAVKSYYLQNYLANAYTYVIKGT-HTGGDLIRFLRTKSEYNAVYAGGGIRL | 567 |
| crylAa   | SSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITA         |     |
| cry1Ac   | SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEV         | 516 |
| cry1Ia   | PNSITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINP         | 553 |
| cry2Aa   | PEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTA              | 532 |
| cry3Aal  | SKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYV             |     |
| cry3Bb   | AEKITQLPVVKAYALSSGASIIEGPGFTGGNLLFLKESSNSIAKFKV            | 555 |
| cry4Aa   | THLTTQIPAVKANSLGTASKVVQGPGHTGGDLIDFKDHFKITCQ               |     |
| cry4Ba   | TDAITQVPAVKSNFLNATAKVIKGPGHTGGDLVALTSNGTLSGRMEIQCK         | 526 |
| cry6Aa   | SHEYTSLPNNFMLSR  | 443 |
| cry7Aa   | PNKITKIPAVKMYKLDDPSTVVKGPGFTGGDLVKRGSTGYIGDIKATVNS         |     |
| cry8Aa   | SDKITQIPAVKGDMLYLGGSVVQGPGFTGGDILKRTNPSILGTFAVTVNG         | 572 |
| cry10Aa  | LDNITQIHALKALKVSSDSKIVKGPGHTGGDLVILKDSMDFR                 | 548 |
| cry16Aa  | ANKITQIPVVKASSINGSISIEKGPGFTGGDLVKMRADSGLTM                | 551 |
| cry19Ba  | PDKIVQIPAVKTNLVGANIIKGPGHTGGDLLKLEYERFLSL                  | 543 |
| cry24Aa  | PDEITQIPAVTAYELRGNSSVVAGPGSTGGDLVKMSYHSVWS                 | 553 |
| cry25Aa  | YDKITQIPATKTVREHPMIKGPGFTGGDLADLSSNSDILQYDLRSD             | 566 |
| cry39Aa1 | PDKITQIPAVKGDYLQYGYVKQGPGHTGGDLVSMIRTDRLGI                 | 539 |
| cry40Aa1 | PDKITQIPAVKAFDISDTGPGQVIAGPGHTGGNVVSLPYYSRLKIRL            | 555 |
|          | •  |     |
|          | ·  |     |
| axmi008  | IINNKTAGQSYRIRFRYAADKAAFFSVYLYPGGWGSNRFVSLEKSYSGNYDDLK     |     |
| cry1Aa   | PLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQ              | 561 |
| cry1Ac   | PIHFPSTSTRYRVRVRYASVTPIHLNVNWGNSSIFSNTVPATATSLDNLQ         | 566 |
| crylIa   | PFAQRYRVRIRYASTTDLQFHTSINGKAINQGNFSATMNRGEDLD              | 598 |
| cry2Aa   | RYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYTVSNVNTTTNNDGVNDNGAR     |     |
| cry3Aa1  | TP-DVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT         |     |
| cry3Bb   | TLNSAALLQRYRVRIRYASTTNLRLFVQNSNNDFLVIYINKTMNKDDDLT         |     |
| cry4Aa   | HSNFQQSYFIRIRYASNGSANTRAVINLSIPGVAELG-MALNPTFSGTDYTNLK     |     |
| cry4Ba   | TSIFNDPTRSYGLRIRYAANSPIVLNVSYVLQGVSRGTTISTESTFSRPNNIIPTDLK |     |
| cry6Aa   | NSNLEYKCPENNFMIYWYNNSDWYNNSDWYNN                           | 475 |
| cry7Aa   | PLSQKYRVRVRYATNVSGQFNVYINDKITLQTKFQNTVETIGEGKDLT           | 591 |
| cry8Aa   | SLSQRYRVRIRYASTTDFEFTLYLG-DTIEKNRFNKTMDNGASLT              | 919 |
| cry10Aa  | VRFLKNVSRQYQVRIRYATNAPKTTVFLTGIDTISVELPSTTSRQNPNATDLT      | 001 |
| cry16Aa  | RFKAELLDKKYRVRIRYKCNYSSKLILRKWKGEGYIQQQIHNISPTYGAFSY       | 503 |
| cry19Ba  | RIK-LIASMTFRIRIRYASNISGQMMINIGYQNPTYFNIIPTTSRDYTELK        | 573 |
| cry24Aa  | FKVYCSELKNYRVRIRYASHGNCQFLMKRWPSTGVAPRQWARHNVQGTFSNSMR     | 616 |
| cry25Aa  | YDDRLTEDVPFRIRIRCASIGVSTISVDNWGSSSPQVTVASTAASLDTLK         | 501 |
| cry39Aa1 | NVY-FPQPLDYRIRIRYSTSSNGYLYIYSPNTKIVYLPPTTLVDGQPTFDPMD      | 221 |
| cry40Aa1 | IPASTNKNYLVRVRYTSTSNGRLLVERWSPSSIINSYFFLPSTGPGDSFG         | 605 |

| axmi008  | YSDFKFAEIITPPLPSSNIQMDVEMQANSFQSDVNVVLDKIEFLPSNTTTLEYEGER    | 678 |
|----------|--|-----|
| cry1Aa   | SGSFRTVGFTTPFNFSNGSSVFTLSAHV-FNSGNEVYIDRIEFVPAEVTFEAEY       | 614 |
| cry1Ac   | SSDFGYFESANAFTSSLGNIVGVRN-FSGTAGVIIDRFEFIPVTATLEAEY          |     |
| cry1Ia   | YKTFRTVGFTTPFSFLDVQSTFTIGAWN-FSSGNEVYIDRIEFVPVEVTYEAEY       |     |
| cry2Aa   | FSDINIGNIVASDNTNVTLDINVTLNSGTPFDLMNIMFVPTNLPPLY              | 633 |
| cry3Aa1  | YNSFNLASFSTPFELSGNNLQIGVTG-LSAGDKVYIDKIEFIPVN                | 652 |
| cry3Bb   | YQTFDLATTNSNMGFSGDKNELIIGAES-FVSNEKIYIDKIEFIPVQL             | 652 |
| cry4Aa   | YKDFQYLEFSNEVKFAPNQNISLVFNRSDVYTNTTVLIDKIEFLPITRSIREDREKQ    | 688 |
| cry4Ba   | YEEFRYKDPFDAIVPMRLSSNQLITIAIQPLNMTSNNQVIIDRIEIIPITQSVLDETENQ |     |
| cry6Aa   |  |     |
| cry7Aa   | YGSFGYIEYSTTIQFPDEHPKITLHLSD-LSNNSSFYVDSIEFIPVDVNYAEKE       |     |
| cry8Aa   | YETFKFASFITDFQFRETQDKILLSMGD-FSSGQEVYIDRIEFIPVDETYEAEQ       | 669 |
| cry10Aa  | YADFGYVTFPRTVPNKTFEGEDTLLMTLYGTPNHSYN-IYIDKIEFIPITQSVLDYTEKQ | 660 |
| cry16Aa  | LESFTITTTENIFDLTMEVTYPYGRQFVEDIPSLILDKIEFLPTN                | 648 |
| cry19Ba  | FEDFQLVDTSYIYSGGPSISSNTLWLDNFSNGPVIIDKIEFIPLGITLNQAQGYD      | 648 |
| cry24Aa  | YEAFKYLDIFTITPEENNFAFTIDLESGGDLFIDKIEFIPVSGSAFEYEGKQ         | 659 |
| cry25Aa  | YESFQYVSIPGNYYFDSAPRIRLLRQPGRLLVDRIEIIPVNFFPLS               | 662 |
| cry39Aa1 | FSAFRVVEVPASFRASVAGYTNFTIEAGFGPVYIDKIEFIPDNTTTLEYEGGR        | 644 |
| cry40Aa1 | YVDTLVTTFNQPGVEIIIQNLDTPINVDKVEFIPVNSTALEYEGKQ               | 651 |
|          |  |     |
| axmi008  | DLEKTKNAVNDLFTN  | 693 |
| cry1Aa   | DLERAQKAVNELFTSSNQIGLKTDVTDYHIDQVSNLVECLSDEFCLDEKQELSEKVKHAK | 674 |
| crylAc   | NLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAK |     |
| crylIa   | DFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAK | 711 |
| cry2Aa   |  |     |
| cry3Aa1  |  |     |
| cry3Bb   |  |     |
| cry4Aa   | KLETVQQIINTFYANPIKNTLQSELTDYDIDQAANLVECISEELYPKEKMLLLDEVKNAK | 748 |
| cry4Ba   | NLESEREVVNALFTNDAKDALNIGTTDYDIDQAANLVECISEELYPKEKMLLLDEVKNAK | 704 |
| cry6Aa   |  |     |
| cry7Aa   | KLEKAQKAVNTLFTE-GRNALQKDVTDYKVDQVSILVDCISGDLYPNEKRELQNLVKYAK |     |
| cry8Aa   | DLEAAKKAVNALFTNTKD-GLRPGVTDYEVNQAANLVECLSDDLYPNEKRLLFDAVREAK |     |
| cry10Aa  | NIEKTQKIVNDLFVN  | 675 |
| cry16Aa  |  |     |
| cry19Ba  | TYDQNANGMYHQNYSNSGYNYNQEYNTYYQSYNN                           | 682 |
| cry24Aa  | NIEKTQKAVNDLFIN  | 674 |
| cry25Aa  | EQENKSVDSLFIN  | 675 |
| cry39Aa1 | DLEKTKN-AVNDLFTN   | 659 |
| crv40Aa1 | SLEKAQDVVNDLFVK  | 666 |

| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | MSPMFTSSTKNTLKIETTDYEIDQAAISIECMSDEQNPQEKIMLWDEIKLAKQLSQSRNL VNFMLTSGAKNMLKLETTDYEIDQMANAIENMSGEQYSQEKMMQWHDIKYAKQLSQARNLMFISNIKNTLKIETTDYEIDQAAISIECMSNEHSSKEEMMLWDEVKQAKQLSWSRNLMFTNGTKNTLKIETTDYEIDQAAISIECMSDEHSPKEKMMLWDEVKRAKLLSQSRNL INTFYANPIKNTLQSELTDYDIDQAANLVECISEELYPKEKMLLLDEVKNAKQLSQSRNV VNALFTNDAKDALNIGTTDYDIDQAANLVECISEELYPKEKMLLLDEVKNAKQLSQSRNV : *: *: ***:*** * :* :* * : * : * : * :       | 60<br>57<br>57<br>60     |
|--|---|--------------------------|
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | LQNGDFSGNDWTFGNDIIIGSNNPIFKGKFLQMRGARDIYGTLFPTYICQKIDESKL LQNGDFEDLFSG-WTTSNQMSIQADNATFKGNYLHMSGARDIYGTIFPTYIYQKIDESKL LYNGDFEDVSNG-WKTSNTIEIRENSPVFKGHYLHMFGARDIDGTLFPTYIYQKIEESKL LQNGDFGDFYGNDWKFGNNIIIGSNNSIFKGNFLQMSGARDIYGTIFPTYIYQKIDESKL LQNGDFESATLG-WTTSDNITIQEDDPIFKGHYLHMSGARDIDGTIFPTYIFQKIDESKL LQNGDFESATLG-WTTSDNITIQEDDPIFKGHYLHMSGARDIDGTIFPTYIFQKIDESKL * ** ***::*: * ***** **::********        | 119<br>116<br>117<br>119 |
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | KPYTRYRVRGFVGSSKDLKLMVTRYGKEIDAIMNVPNDLAYMQPNPSCGDYRCESSS KPYTRYLVRGFVGSSKDLELMVMRYGKEIDTVMNVPNDIPYVPSMPVCNELYDGQQPYPN KPYTRYRVRGFVGSSKDLKLMVTRYGKEIDAMMNVPNDLAYMQPTPSCGDSRCESSS KPYTRYRVRGFVGSSKDLRLMVTRYGKEIDAMMNVPNDLAYMQPNPSCGDSRCESSS KPYTRYLVRGFVGSSKDVELVVSRYGEEIDAIMNVPADLNYLYPSTFDCEGSN KPYTRYLVRGFVGSSKDVELVVSRYGEEIDAIMNVPADLNYLYPSTFDCEGSN ****** ******************************                        | 179<br>173<br>174<br>172 |
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | QYVSQGYPTP-TDGYAPDMYACPQNIDRKHVKCHDRHPFDFHIDTGEVDTNTNVGIDVLL RHVGYYNPMP-VSQPSYTSDTCQCTPGKKHVVCHDSHQFKFHIDTGEVDYNTNLGIWVLF RYVSQGYPTPVTDGYASGRYACQSNRGTKHVKCHDRHPFDFHIDTGELDTNTNVGIDVLF QYVSQGYPTP-TDGYAPDRYACPSSSDKKHVMCHDRHPFDFHIDTGELDTNTNVGIDVLF RCETSAVPAN-IGNTSDMLYSCQYDTGKKHVVCQDSHQFSFTIDTGALDTNENIGVWVMF RCETSAVPAN-IGNTSDMLYSCQYDTGKKHVVCQDSHQFSFTIDTGALDTNENIGVWVMF:                                      | 238<br>233<br>233<br>231 |
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | KISNPDGYATVGNLEVIEEGPLTGEALAHVKQKEKKWKQHMEKKRWETQQAYDPAKQAVD KISSPDGYATLDNLEVIEEGPVRGEAVTHVKQKEKKWNQQMEKKRMETKRVYDRAKQAVD KISNPDGYATLGNLEVIEEGPLTGEALTHVKQKEKKWKQHMEKKRWETQQAYDPAKQAVD KISNPDGYATLGNLEVIEEGPLTGEALTHVKQKEKKWKQHMEKKRWETQQAYDPAKQAVD KISSPDGYASLDNLEVIEEGPLDGEALSRVKHMEKKWNDQMEAKRSETQQAYDVAKQAID KISSPDGYASLDNLEVIEEGPLDGEALSRVKHMEKKWNDQMEAKRSETQQAYDVAKQAID ***.****::.**                         | 298<br>293<br>293<br>291 |
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | ALFTNEQELHYHITLDHIQNADRLVQSIPYVYHNWLPNAPGMNYDVYQELNARIMQGY ALFTGEELNYDVTLSHIKNADDLVQSIPYVHNEWLPDFPGMNYDIYQELNARIMQAR ALFTNEQELHYHITLDHIQNADRLIQAIPYVYHAWLPDAPGMNYDGYQGLNARIMQAY TLFTNEQELHYHITLDYIQTLIDWYSRFPIYTMTGYRDAPGMNYDGYQGLNARIMQAY ALFTNVQDEALQFDTTLAQIQYAEYLVQSIPYVYNDWLSDVPGMNYDIYVELDARVAQAR ALFTNVQDEALQFDTTLAQIQYAEYLVQSIPYVYNDWLSDVPGMNYDIYVELDARVAQAR :***. : *::. ** : : *:. ** : : *:.**           | 355<br>351<br>351<br>351 |
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | NLYDARNVITNGDFTQGLQGWHATGNAAVQQMDGASVLVLSNWSAGVSQNLHAQDHHGYV YLYDARNVITNGDFAQGLQGWHAEGKVEVQQMNGTSVLVLSNWSAGVSQNLHVQHPHGYL NLYDARNVITNGDFTQGLTGWHAAGKAMVQQMDGASVLVLSNWSAGVSQNLHVQEHHGYM NLYDARNVITNGDFTKGLQGWHAAGKAAVQQIDGASVLVLSNWSAGVSQNLHAQDHHGYM YLYDTRNIIKNGDFTQGVMGWHVTGNADVQQIDGVSVLVLSNWSAGVSQNVHLQHNHGYV YLYDTRNIIKNGDFTQGVMGWHVTGNADVQQIDGVSVLVLSNWSAGVSQNVHLQHNHGYV ***:**:*::::::::::::::::::::::::::::: | 415<br>411<br>411<br>411 |

| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | LRVIAKKEGPGKGYVTMMDCNGKQETLKFTSCEEGYMTKTVEVFPESDRVRIEIGETEGT LRVSAKKEGSGKGYVTRMSCNGKQETLTFTSCDGGYMTKTVEVFPESDRVRIEIGETEGS LRVIAKKEGPGKGYVTMMDCNGNRETLKFTSCEEGYMTKTVEVFPESDRVRIEIGETEGT LRVIAKKEGPGKGYVTMMDCNGNQETLKFTSCEEGYMTKTVEVFPESDRVRIEIGETEGT LRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEEGYITKTVDVFPDTDRVRIEIGETEGS LRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEEGYITKTVDVFPDTDRVRIEIGETEGS *** ***** .*: *** * .*: :: ************ | 475<br>471<br>471<br>471 |
|--|---|--------------------------|
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | FYIDSIELLCMQGYDNNNNLHTGNMYEQSYNGNYNQNTSDVYYQGYTNNYNQDSSNMYNQ FYIESIELICMNGYTSNNNQNMSNMYDQSYSGNYSQNTSDMYDQGGSVAKFEK FYVDSIELLCMQGYASNNNPHTGNMYGQSYNGNYNQNTSDVYHQGYTNNYNQNSSNMYNQ FYVDSIELLCMQGYASNNNPHTGNMYGQSYNGNYNQNTSDVYHQGYTNNYNQNSSNMYNQ FYIESIELICMNE  | 528<br>531<br>531<br>484 |
| axmi008-orf2<br>cry19Aa-orf2<br>crybun2orf2<br>crybun3orf2<br>cry4Aa<br>cry4Ba | NYTNNDDLHSGCTCNQGHNSGCTCNQGYNR 561 E529 NYTHNDDLHSGCTCNQGHNSGCTCSQG558 NYTHNDDLHSGCTCNQGHNSGCTCSQG558   |                          |